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Perfect score:
Sequence:
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      A_Geneseq_1101:*
1: /STDS1/gcqdata
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Omery Match Length DB	enuth		10	bescription
_ ;	166	100.0	30	21	AAY64618	Peptide included i
K.	166	100.0	4	2.	AAY: 4118	Ribonuclease S-pro
.ند	166	100.0	4	23	AAW59680	Ribonuclease S.pr.
4	166	100.0	- ] (-	_	AAW71707	Synthetic S(+5)-pa
5	166	100.0	24	6	AAR49151	Wild-type bovine p
Ť	166	100.0	24	20	AAWF1768	Talvine RWAS poptial
7	166	0.001	2.4	K	AAY69974	kNAS protein. Bos
α.	166	100.9	928	25	AAEUS749	Chimeric S peptide
9	158	95.2	124	<del>-</del>	AAW 45108	dovine pancreatic
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ondinan' Bress s	time supione esti	Special Lance and	Toplide #1501 one	en in a dia orași să	Camura protected CANC	immin protess (AN)	.nmunoproteca FANG	Crimuroproteci TANC	Andiotenia 148 ESI	FGP:drangle relin 1	Lindipolentin i PSF i	IGF andioged.in fus	Haman secretal pro	Finan ingiraction	Steament of a ring	Fectombinant four 30	Androgenin derica.	Ar degenin detail.	Analogenin bit.v.	Ataliodonin piiAl	Synthetic human an	Buman andisestin p	Mitant Ang. estin.	Sequence of tradi	A: thS itivi: quitus	Cuman secretaring	Sene & human seeme	Haman secrettii	Buman color ancer	Hollian Secretoi pro	Moditiod NET page	Mutadenized public	with about the second of

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AAY84618;

Production of a semi symble of the activate one of target protein tused to a protein sport of a mexicolection, cleaving the tust o	WHI. 2009 2931 0 /25.	Xu M, Evans TC:	(NEWE ) NEW ENGLAND BIOLABS INC.	30-SEP-1998; 980S-0102413.	30-SEP-1999; 99WO-US22776.	06-APR-2000.	W0200018881-A2.	Unidentified.	PALACTER TARREST FOR PARTIES OF THE PROTECTION O	Repuide included in ligation reactions between a MBP and	Commission (Constitution)
um vitro ry producisa a mesi (intelm),									dera protein:	H a MBP and MXB.	

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                     The present incention describes a cross linked enzyme component (A), which (i) has an inserted enzyme reconsition site (ERS) in a polypeptide of the component; and loss at least one covalent intractant cross link between amino acid side eigens of the polypeptide. The component forms an enzymatically active complex with a second orzyme component forms an enzymatically active complex with a second orzyme.
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                                                                                                                                                                                                                                                                                                                                                  New crease linked encyme compensates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BORE ) BORRESTANDE MARSHES MANAGED (SECTION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this to an in size expresses protein isolated using a modified intern. The present sequence represents a populae included in light on routions between a mallose binding protein (MMC) and a maltose binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a method for fusing an expressed protein with a peptide. The method comprises general find at least one 2 ferminal thiosafter tapast forest and at least one tapast peptide hazing a specific d N terminal and lighting the target peptide to the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contract This on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIV: protesse cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross linked polypeptibe assay: cross-linked enzyme component; cleavage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribonuclease S protein
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complex prior to charage. The complex has enzymentic activity which is
                                                                                                                                                                                                                                                                                                                       complement with other enzyme components to form an active enzyme
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100.0% Pred. No. 1.7e 19;
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guery Match | 190, 00 Score 156; DR 20;
Hest Local Similarity 190, 00 Pred, No. 8,50-19;
Marchas 40; Copsored to 10 Mismarches 10;
                                               polypeptide. The CLM compaises an encymatically cleavable site. The produced is converted to a the apeutically more effective form upon cleavage of this site. The artivated form of the produce may have any desired toological activity including activity in suppression of
                                                                                                                                              converted to a therapeutically more effective form upon cleavage of
the ERS. (B) cross Linked profing, which: (i) has an inserted ERS in
polypeptide of the prodrag and (ii) has at least one cross linking
mojety (CLM) cosalently based between amino acid side chains of the
                                                                                                                                                                                                                                                has an inserted enzyme recomition site (ERS) in a polypeptide of
prodrug; and (ii) has at least one covalent intrachain cross-link
between amino acid side chains of the polypeptide. He prodrug is
                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide prodrugs—include, e.g. an inserted enzyme recognition site and a covarient intrachain cross link between amino acid side chains of the polypeytide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   different from that of bota galactosidase. The component may be used for measurement of substances in biological samples, it is especially useful for measurement of enzymes (e.g. professes, particularly vital, phosphatases, qycosidase, midase and esterase) in clinical samples, or for measurement of target polymucloolides. Assay methods using the new components exhibit extremely low inherent background signals, due to reduction or inhibition of complementation of enzyme components prior to cleavage. The present sequence represents a profein from the present
desired biological activity including activity in suppression of inflammatory or immunological activity, promotion of arowth or a direct cytotoxic effect on target earls. Following cleavage of the ERS, the
                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 6: 44pp: Earlish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; human immunodeticlency virus; cyclised prodrug; inhibition; coratently cross-linked; elegable site; suppression; inflammatory; immunological activity, great, cytotoxic effect.
                                                                                                                                                                                                                                                                                                          The present invention describes: (A) cross-linked product, which: (i)
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prodrym reassembles internative by unfolding or retolding, or reassembles

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Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of transposic plants having a desired phenotype - by using a pair of parent plants which each produce a polypeptide complement each other when crossed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richisos burginos (1949) interne prigmentas chais scrittia, planatype transquain plant; bytrid good; male specifo plant; active escymos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE SHEARS PTY LTD.
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milarity 190.0%; Pred. No. 8.5e 19;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98W0-CB00542.
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AAR49151
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                                                                      carrying the Rhase A chNA was deletated to the b A game uning PCE and the '' and ' pair \mathbb{R} 4 . . . SD4 (AAQES991), respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim a novel mutant part of its which differs from the wile type of the (A4.
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Sequence
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Query Mutch 106. %: Rest Local Similarity 109. %. Matches 3:: Conservative

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MNAS protecto
              Protein separate database biological function determination; energial of principal extension activity; protein function determination;
                                                                          PNAS profeshi
                                                                                                                   DOOZ ANV FT
                                                                                                                                                          AAYAMA 24;
                                                                                                                                                                                                AAY69974 standard; protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           presumption of protein and polypeptide having biological functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structure of protein, and includes retrieval and evaluation of high
homologous relationship for the determination of mostly resembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the biological information for each amino acid residue. The database is useful for determination of unknown biological function of a protein or polypeptide based on the homology of amino acid sequence, e.g. steries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biological function with added a score on importance of expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1: Fig U Hpp: Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TYAK ) TYAKU MUNCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 APP 1511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHFR: diligatoralic acid reductase; protein tunction: trypsin; bozine; ribonuclease; myodlobin; database; homolody; resemblance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine FNAS peptide transment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                information for amino acid sequence of protein with at least 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 APR 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 1961 1 1988
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hes to Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is used in the creation of a database containing the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The database allows for correct and rapid retrieval and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AA;
                                                                                                                   (lirst entry)
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100.0%; Fred. No. 1.1e
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                                                                                                                                                                                                                                                                                                                                                                                                                Lamqth 124;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preparind an alignment between as sequences contained in the database and those of the unknown pulypeptide. This is represented as the homology amongst various sites, each being identified as having a high score of importance in determining potential biotogical functions. The method is used to enable an etticient estimation of the biological particular generation as sequences. Suitable proteins can then be isolated and purified by various means. This could be of considerable use in a biological and
                 Region
                                                                        Chimeric
                                                                                         Chimerie
                                                                                                                           Spep-CBD-Sprot; bovin
                                                                                                                                            chimeric protein: S peptide cellulose binding domain-S protein;
                                                                                                                                                                                                 Polysaecharide medification: polysaecharide binding domain; PBD; paper;
                                                                                                                                                                                                                                   Chimeric S peptide-cellulose binding domain-S protein
                                                                                                                                                                                                                                                                                                                                                AAE05749 standard; Protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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the known block-gion. Junetieue, The invention also relates to a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid (aa) sequences of preferrs of which Lor more biological functions are known. The database are contains additional information on the score
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                                                                                                                                                               wet strength: durability: clasticity: cellulose binding domain: CBD;
                                                                                                                                                                                                                                                                      24 SEP-2001 (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accurate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medical context. The computerised procedure is efficient, fast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a database containing information on the amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the KNAS protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An efficient, accurate and rapid computer database for estimating
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAYKITQANKHIIVACIBBNEYVEVHEDASV 30
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                                                                                                                                                                                tibor; textile; biological crosslinker; mechanical property
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomioka N,
                                                                    - Bos sp.
                                                                                     - Clostridium celialogorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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 /acct c
                                Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 166; DB 21;
100.0%; Pred, No. 1.1e-18;
valive 0; Mismatches 0;
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"This region is derived from C.
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AAW (5108
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Best Local Similarity
Matches 30, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of a polysarcharide containing material baying at least one desired structural, closical, physical, electrical and/or mechanical
              AAW 51 08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invertion relates to methods and compacitions for cross-
linking addor modifying the properties of polysarcharide materials.
The method involves treating the polysarcharide structure with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200144091-A2
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                                                     AAW'5108 standard
                                                                                                                                                                                                                                                                                                                                                                  Note: This sequence is stated to be the same as that shown as SEQ IN Nor 10 in the empression listing of the specification, However this sequence has 2 additional residues at its C-terminal.
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